Interaction of L-phenylalanine with a phospholipid monolayer at the water-air interface

Elizabeth C. Griffith[1], Russell J. Perkins[1], Dana-Marie Telesford[2], Ellen M. Adams[2], Lukasz Cwiklik[3,4], Heather C. Allen[2], Martina Roeselová[4], Veronica Vaida[1]**

Supporting Information

METHODS

Brewster Angle Microscopy – BAM images shown in Figure S6 were collected on a BAM instrument similar to the one described in the main text with slight alterations: a 17 mW p-polarized 633 nm illumination source (Research Electro-Optics), a Nikon 20x infinity corrected super long working distance objective, and a back illuminated anti-reflective CCD (Andor model DV412-BV)

MD Simulation Insertion Procedure – The following procedure was used to create the initial configuration for the simulations of aqueous solution of L-phenylalanine (Phe) between two monolayers of DPPC. A pre-equilibrated system consisting of a water slab (6876 water molecules) with a DPPC monolayer (64 DPPC molecules) on either air-water interface was visualized in VMD and used as the starting configuration. The dimensions of the entire periodic box were 6.69 x 6.69 x 28 nm. The middle portion of the water slab, i.e., a 2 nm-thick slice containing only water molecules, was removed, leaving the two solvated DPPC monolayers and a void between them (System A, Figure S1).

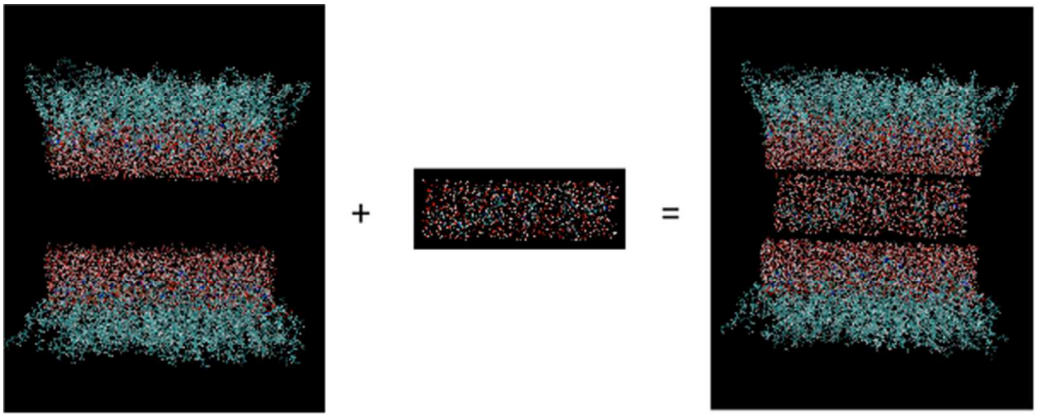

Figure S1: Snapshots during insertion procedure.

Using GROMACS, a 6 x 6 x 1.75 nm box (i.e., of slightly smaller size than the void in System A) was generated, containing the desired number of Phe molecules. The molecules were positioned randomly within the box in such a way as to avoid overlap between them, and subsequently solvated with water (System B, Figure S1). Both systems were then combined by inserting the box of solvated Phe molecules between the two hydrated monolayers of DPPC and centering it within the void. The resulting configuration is shown in Figure S1. Finally, a short energy minimization was performed with GROMACS to prevent close contacts between atoms, followed by a 10ns equilibration NVT run at T=310 K. Any void space remaining in the system after the insertion of the box of Phe solution between the two DPPC monolayers was quickly eliminated within the first few tens of picoseconds of the simulation run.

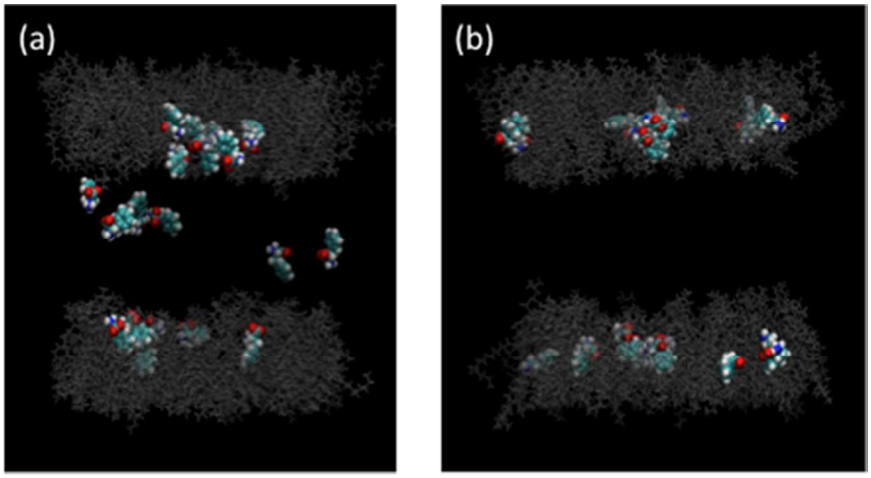

Figure S2: Snapshot after 20 ns of simulation of (a) zwitterionic Phe and (b) neutral Phe, DPPC system. DPPC molecules are shown in gray and water molecules are removed for clarity.

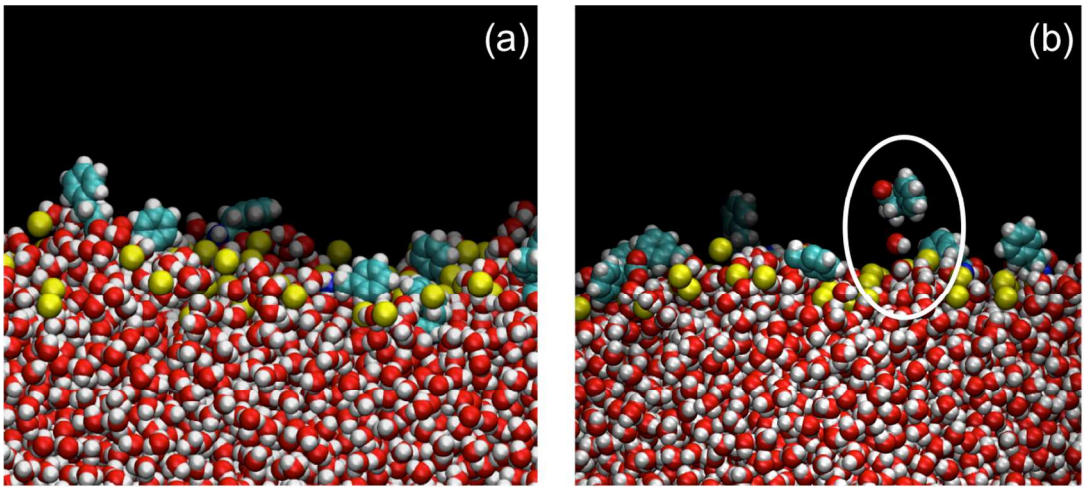

Figure S3: Snapshot from zwitterionic (a) and neutral (b) Phe within the DPPC film (only C2 atom from DPPC molecules are shown for clarity) illustrating occasional dehydration of neutral Phe molecules within film (indicated by white circle) but consistent solvation of headgroups of zwitterionic Phe throughout the simulations.

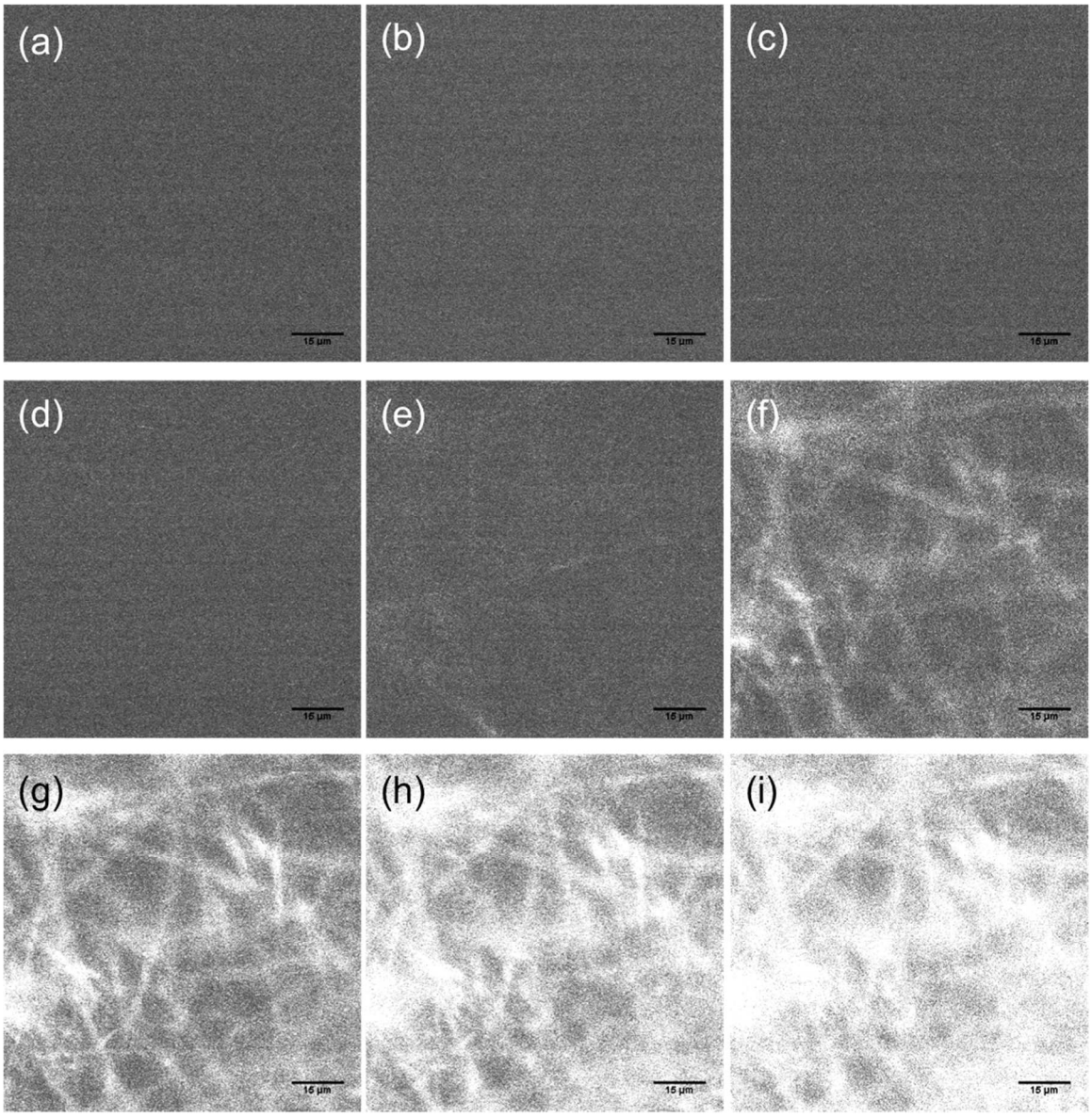

Figure S4: Confocal microscope images over time during drying out of 120 mM Phe solution forming fibrils. The images are taken at the following times after deposition: (a) 1 minute, (b) 7 minutes, (c) 8 minutes, (d) 8.5 minutes, (e) 9 minutes, (f) 9.5 minutes, (g) 10 minutes, (h) 10.5 minutes, (i) 11 minutes. Scale bars represent 15 μm.

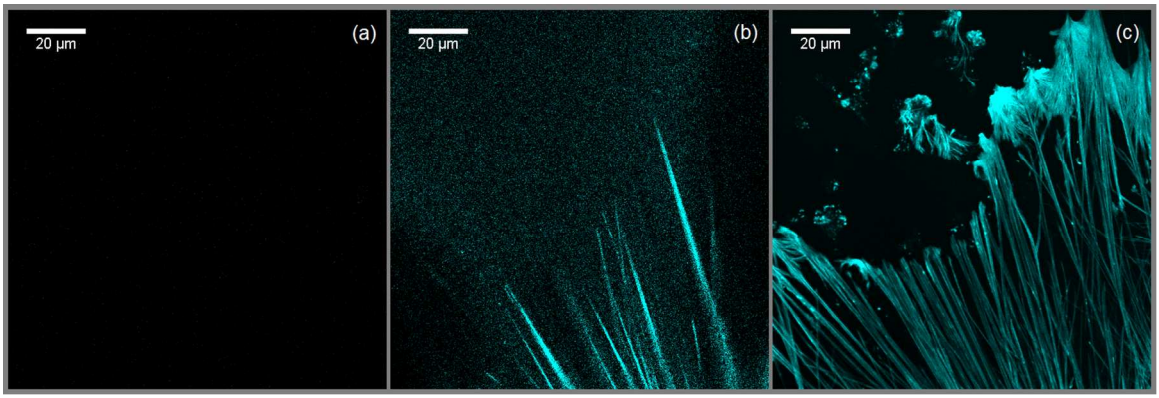

Figure S5: Confocal microscope images of 2.5 mM Phe solution (a) immediately after deposition on slide, (b) fibrils forming in solution as the drop dries and shrinks and (c) dried fibrils in better focus. Scale bar represents 20 µm.

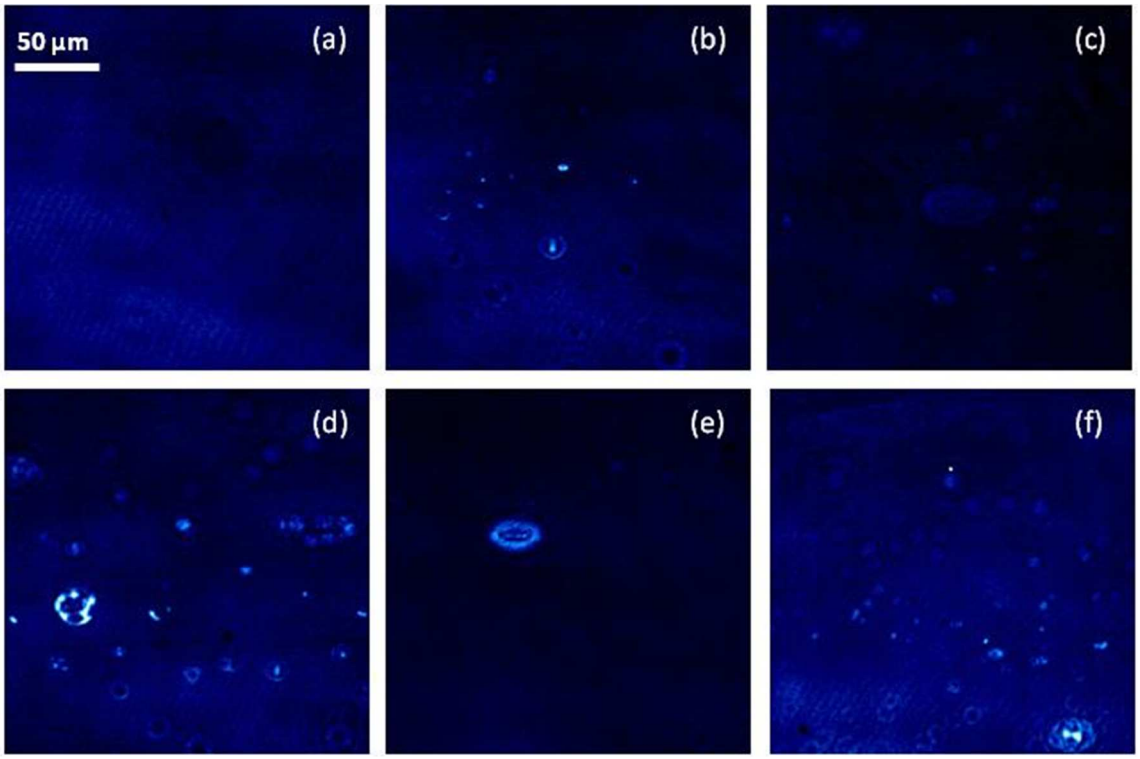

Figure S6: BAM images of 2.5, 10 and 20 mM Phe only aggregates at the bare water surface (a) and (b) 2.5mM Phe at 0 and 16500 s, (c) and (d) 10 mM Phe at 0 and 16500 s, (e) and (f) 20 mM Phe at 0 and 16500s. Scale bar represents 50µm.

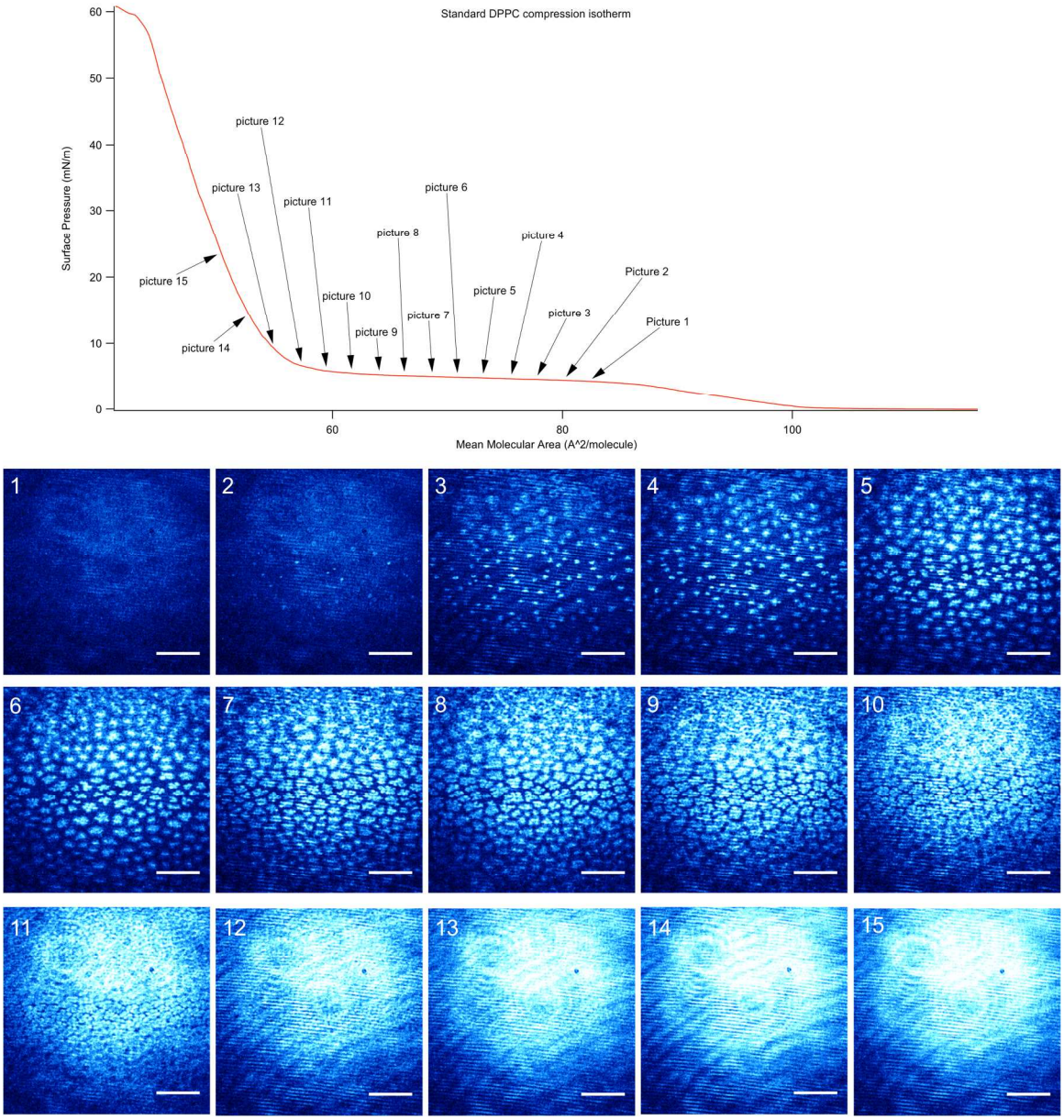

Figure S7: Isotherm of DPPC deposited on water with corresponding BAM images in different phases throughout its isotherm as indicated.

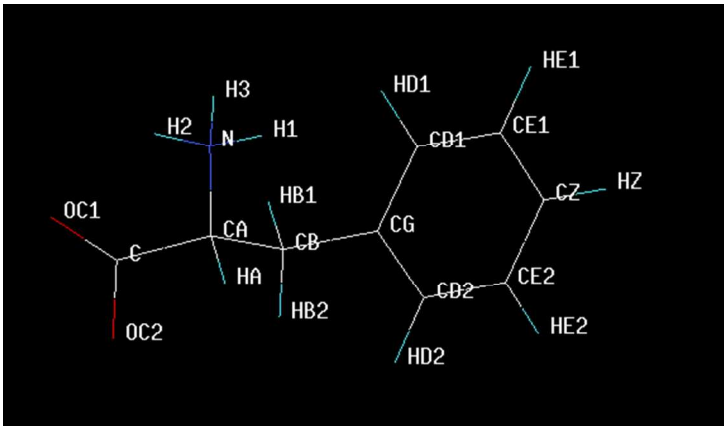

Figure S8. Atom names for zwitterionic Phe

Table S1: Atomic types and charges for zwitterionic Phe. Atom names correspond to Fig. S8.

Atom name	Amber ff03 atom type	Charge
N	N3	-0.335478
H1	H	0.266212
H2	H	0.266212
H3	H	0.266212
CA	CT	0.003747
HA	HP	0.098054
CB	CT	-0.369740
HB1	HC	0.127679
HB2	HC	0.169801
CG	CA	0.237468
CD1	CA	-0.209531
HD1	HA	0.129611
CE1	CA	-0.122457
HE1	HA	0.131357
CZ	CA	-0.129696
HZ	HA	0.128047
CE2	CA	-0.122457
HE2	HA	0.131357
CD2	CA	-0.209531
HD2	HA	0.129611
C	C	0.678048
OC1	O2	-0.632264
OC2	O2	-0.632264

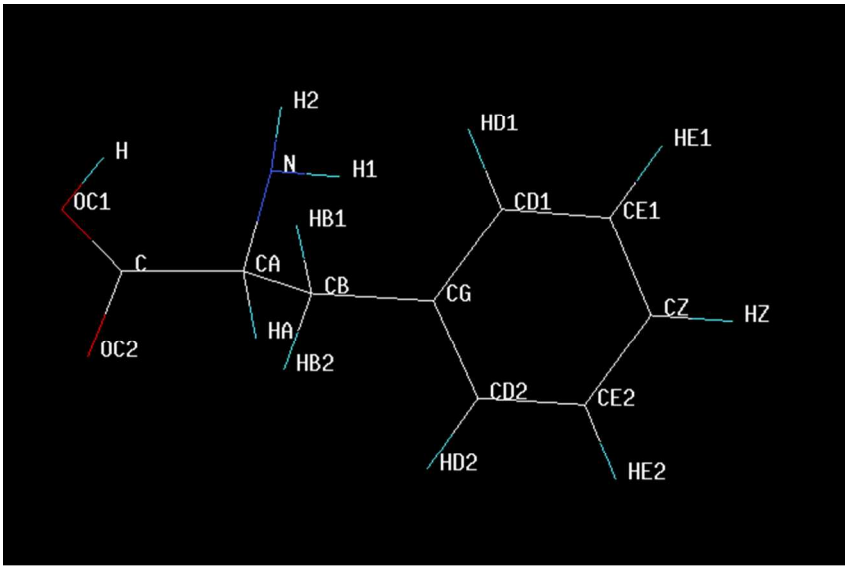

Figure S9. Atom names for neutral Phe

Table S2: Atomic types and charges for neutral Phe. Atom names correspond to Fig. S9.

Atom name	Amber ff03 atom type	Charge
N	N3	-0.841199
H1	H	0.326533
H2	H	0.326533
CA	CT	0.238852
HA	HP	0.025766
CB	CT	-0.257047
HB1	HC	0.083838
HB2	HC	0.057174
CG	CA	0.171940
CD1	CA	-0.169748
HD1	HA	0.108205
CE1	CA	-0.117582
HE1	HA	0.121796
CZ	CA	-0.122945
HZ	HA	0.119201
CE2	CA	-0.117582
HE2	HA	0.121796
CD2	CA	-0.169748
HD2	HA	0.108205
C	C	0.550381
OC1	OH	-0.484507
OC2	O	-0.431490
H	HO	0.351627